

Final report

Conservation Genomics: amalgamation of conservation genetics and ecological and evolutionary genomics (ConGenOmics)

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Populus spp. (poplars, aspens, cottonwoods) are a group of northern hemisphere trees of great commercial and scientific interest. A few model species of the genus, including *Populus trichocarpa* and *P. tremula*, the Aspen, are intensely studied. However, considerably less is known on the ecologically relevant *P. alba* (White poplar), a close relative of *P. tremula*. *Populus alba* is a key pioneer and ecological foundation species. Much of the molecular ecology and evolutionary genomics research in the Lexer laboratory at the University of Fribourg, Switzerland, focuses on the evolutionary dynamics of *P. alba*, including its frequent hybridization events with *P. tremula*. The proposed short research visit grant has thus provided an optimal opportunity for scientific exchange between the P. Ingvarsson laboratory in Umea, Sweden, which is deeply involved in sequencing the genome of *P. tremula* and analyzing population genomic patterns particularly in Northern Europe, and the Lexer lab with a focus on Central and Southern European *P. alba* including hybrid zones with *P. tremula*. We hence thank the European Science Foundation for funding a short visit which was undertaken between April 23rd 2012 and May 5th 2012.

As aimed for in the granting guidelines, we considered the exchange of genomic resources a major aim of this short research visit. The undertaken research visit not only succeeded in providing an excellent opportunity for intense scientific exchange between researchers involved in genome sequencing and population genomics of *P. tremula* as studied in the laboratories of P. Ingvarsson and colleagues and the applicant, whose focus is on *P. alba* population genomics. Our scientific discussions also included a seminar held by the applicant on *Populus* population genomics, in which funding from the ESF was gratefully acknowledged. As per the intent of the funding intent, the research visit also provided an opportunity to directly exchange genomic resources: The as yet unpublished early-version of the *Populus tremula* assembly was made available to the Lexer laboratory. At the same time, color space whole genome re-sequencing data from the Lexer lab was made accessible for training purposes to scientists at Umea University.

One of the major aims of the application was to establish robust SNP selection and validation criteria and to ultimately compare annotated SNP frequencies in *P. alba* (data from Lexer lab) with *P. tremula* (data from Ingvarsson lab). True to form, we focused a large fraction of our discussions on implementing the correct error structures into reference mapping and SNP calling procedures – the key steps critical to meaningful population genomic analyses. For this, we selected a fraction of the *P. alba* genome – the beginning of

the putative incipient *Populus* sex chromosome – and optimized analysis procedures using different reference mapping, re-alignment and SNP calling software. Here, we reference mapped *P. alba* data both against the publically available *P. trichocarpa* genome and also against the *P. tremula* genome currently under development in Umea. An approximately 25% increase in mapping success (compared to *P. trichocarpa* reference mapping) illustrates the value of using the current *P. tremula* assembly, but we also observed that the currently available *P. tremula* assembly still consist of several thousand scaffolds for the region of interest, making direct comparisons on genomic organization of *P. tremula* and *P. alba* with *P. trichocarpa* difficult. We shall repeat these analyses using computational scripts developed during the research visit as soon as a more condensed *P. tremula* assembly is available. Analysis strategies acquired and the scientific discussions directly helped to stimulate work on the *P. tremula* assembly and were also implemented in ongoing work in the Lexer laboratory using the *P. trichocarpa* genome as reference for the *P. alba* conservation genomics research.

Taken together, the applicant's research stay was deemed highly successful in scientific exchange, including that of genomic resources and particularly in acquired knowledge on bioinformatic analysis strategies for selecting and calling SNPs, and also developed perspectives for future work. We will acknowledge funding of the European Science Foundation in a future publication on the organization of the incipient sex determination region using Solid 4 whole genome resequencing data. It is anticipated that the knowledge gained during this ESF-funded training visit will also aid the teaching of PhD and Master students in population and conservation genomics in both countries involved, Switzerland and Sweden. We look forward to communicating more detailed results of this training visit in upcoming ESF ConGenOmics events, if the opportunity arises.